

5'	GAC	GTG	TTT	GGC	AGC	GGG	ACG	CAC	CAT	TTC	AGT	TGT	GTT	CTT	GGT	TCA	TTT	CGT	54
	9	18	27	36	45														
	63	72	81	90	99	108													
GTC	TCG	CGC	ATG	TTT	CCT	AGA	GTC	TCG	ACG	TTT	CTA	CCT	CTT	CGC	CCC	CTT	TCC		
			M	F	P	R	V	S	T	F	L	P	L	R	P	L	S		
	117	126	135	144	153	162													
CGC	CAC	CCT	TTG	TCC	TCT	GGA	AGC	CCG	GAG	ACA	TCA	GCG	GCT	GCG	ATT	ATG	CTA		
R	H	P	L	S	S	G	S	P	E	T	S	A	A	A	I	M	L		
	171	180	189	198	207	216													
CTC	ACT	GTT	CGG	CAC	GGA	ACA	GTC	AGG	TAC	CGC	AGT	TCA	GCG	CTG	TTG	GCC	CGG		
L	T	V	R	H	G	T	V	R	Y	R	S	S	A	L	L	A	R		
	225	234	243	252	261	270													
ACA	AAA	AAT	AAC	ATC	CAA	AGA	TAT	TTT	GGC	ACT	AAC	AGT	GTG	ATC	TGT	AGC	AAG		
T	K	N	N	I	Q	R	Y	F	G	T	N	S	V	I	C	S	K		
	279	288	297	306	315	324													
AAA	GAT	AAG	CAG	TCT	GTT	CGA	ACT	GAG	GAG	ACT	TCC	AAG	GAG	ACT	TCA	GAG	AGC		
K	D	K	Q	S	V	R	T	E	E	T	S	K	E	T	S	E	S		
	333	342	351	360	369	378													
CAA	GAC	AGT	GAA	AAG	GAA	AAT	ACG	AAA	AAA	GAC	TTG	TTA	GGC	ATT	ATT	AAG	GGC		
Q	D	S	E	K	E	N	T	K	K	D	L	L	G	I	I	K	G		

FIGURE 1A

387	ATG AAA GTT GAA TTA AGC ACA GTA AAT GTA CGA ACA ACA AAG CCC CCC AAA AGA	396	405	414	423	432
	M K V E L S T V N V R T T P P K R					
441	AGA CCA CTT AAA AGT TTG GAA GCT ACA CTT GGC AGG CTT CGA AGA GCT ACA GAA	450	459	468	477	486
	R P L K S L E A T L G R L R R A T E					
495	TAT GCT CCA AAG AAG AGA ATT GAG CCC CTG AGT CCT GAG TTG GTG GCA GCT GCA	504	513	522	531	540
	Y A P K K R I E P L S P E L V A A					
549	TCT GCT GTG GCA GAT TCT CTC CTT TTT GAT AAG CAA ACA ACC AAG TCA GAG CTG	558	567	576	585	594
	S A V A D S L P F D K Q T T K S E L					
603	CTG AGC CAG CTC CAG CAG CAT GAG GAA GAG TCA AGG GCA CAG AGA GAT GCA AAG	612	621	630	639	648
	L S Q L Q Q H E E E S R A Q R D A K					
657	CGA CCT AAA ATT AGT TTC AGT AAC ATA ATA TCA GAT ATG AAA GTT GCC AGA TCT	666	675	684	693	702
	R P K I S F S N I I S D M K V A R S					
711	GCT ACA GCT AGA GTT CGT TCA AGA CCA GAG CTT CGG ATT CAG TTT GAT GAA GGC	720	729	738	747	756
	A T A R V R S R P E L R I Q F D E G					

FIGURE 1B

1134

FIGURE 1C

1143	1152	1161	1170	1179	1188
CTT TCC AAA AAC CCA TAT CTT AGT GTT AAA CAG AAG GTT GAA CAC ATA GAG TGG					
L S K N P Y L S V K Q K V E H I E W					
1197	1206	1215	1224	1233	1242
TTT AGA AAT TAT TTT AAT GAA AAA AAG GAT ATT CTA AAA GAA AGT AAC ATA CAG					
F R N Y F N E K K D I L K E S N I Q					
1251	1260	1269	1278	1287	1296
TTC AAT TAA GAC CAT GGA AAT TTT TAT TTC AAA CAA TTA GAG ATG GAT ATT ACA					
F N					
1305	1314				
ACT AAA TAA AAT AAT TGC 3'					

FIGURE ID

1 MFPRVSTFLPLRPLSRHPLSSGSPETSA AAIMLLTVRHGT 035842
1 MLHRIPAFLRPRFSGLP LSCGNRDVSV A - -VL PAAQSGA GI 1272669

41 VYRSSALLARTKNNIQRYFGTNSVICSKKDKQSVRTEET 035842
39 VR - - - - -TENNIO RHFC TSR SICSKKVDQSV PAN EI GI 1272669

81 SKETSESQDSEKENTKKDLLGI IKGMKVELSTVNVRTTKP 035842
70 SQAAESQGRGKETLKKDLLDI IKDMKVDLSTANVKTPKP GI 1272669

121 PKRRPLKSLEATLGRRLRRATEYAPKKRIEPLSPELVAAAS 035842
110 RGEKPSASLEATVDR LQAPEDPFPKKRNELSPPELVAAAS GI 1272669

161 AVADSLPFDKQTTKSEL LSQLQQHEEESRAQRDAKRPKIS 035842
150 AVADSLPFDKQTTKSEL LROLQQHEEELRAQKDREKRRIS GI 1272669

201 FSNISDMKVARSATARVRSRPPELLRIQFDEGYDNYPGQEK 035842
190 FTHIISNMKI AKSPS GRASTRPQH QIOFDEDM DSSLKQEK GI 1272669

241 TDDLLKKRKNIFTGKR LNI FDMMAVTKK EAPETDTS PSLWDV 035842
230 PTDFRKRKYLFK GKRLSIFADKAFAD EPPPEASPSLWEI GI 1272669

281 EFAKQLATVNEQPLONGFEEELIQWTKEGKLWEPFINNEAG 035842
270 EFAKQLASVADOPFENGFEEMIQWTKEGKLWEPFINNEAG GI 1272669

FIGURE 2A

321 FDDDDGSEFHEHIFLEKHLSEFPKQGPRI RHFMELVTCGLSK 035842
310 LDDDDGSEFHEHIFLDKYLEDFPKQGPRI RLFMELVTCGLSK GI 1272669

361 NPYLSVKQKVEHIEWFRNYFNEKKDILKESNIOFN 035842
350 NPYLSVKQKVEHIEWFRNYFNEKRDILKENNIAFT GI 1272669

FIGURE 2B